

AMENDMENTS TO THE SPECIFICATION:

Please replace the title found on lines 1-3 of page 1 of the specification with the following title:

METHODS FOR IDENTIFYING GLUCOCORTICOID RECEPTOR MODULATORS

Please amend the paragraph beginning on line 4 of page 20 as follows:

Figure 16 is a depiction of the overlay of the GR/Dex crystal structure (grey) with the GR/A-222977 (white) comparing the geometries of the ligands and the relative locations of the amino acid side chains that comprise the GR expanded binding pocket. Figure 17 is a sequence alignment of amino acid residues comprising the ligand binding domains of GR (amino acids 527-777 of SEQ ID NO:4), MR (SEQ ID NO:12), PR (SEQ ID NO:13) and AR (SEQ ID NO:14).

Please amend the paragraph beginning on line 5 of page 76 as follows:

Programs such as RASMOL (Biomolecular Structures Group, Glaxo Wellcome Research & Development Stevenage, Hertfordshire, UK Version 2.6, August 1995, Version 2.6.4, December 1998, © Roger Sayle 1992-1999) and Protein Explorer (Version 1.87, July 3, 2001, © Eric Martz, 2001 and available online at www.umass.edu/microbio/chime/explorer/index.htm ~~http://www.umass.edu/microbio/chime/explorer/index.htm~~) can be used with the atomic structural coordinates from crystals generated by practicing the invention or used to practice the invention by generating three-dimensional models and/or determining the structures involved in ligand binding. Computer programs such as those sold under the registered trademark INSIGHTII® (available from Accelrys of San Diego, California, United States of America) and the programs GRASP (Nicholls et al., (1991) *Proteins* 11: 281) and SYBYL™ (available from Tripos, Inc. of St. Louis, Missouri, United States of America) allow for further manipulations and the ability to introduce new structures. In addition, high throughput binding and bioactivity assays can be devised using purified recombinant protein and modern

reporter gene transcription assays known to those of skill in the art in order to refine the activity of a designed ligand.

Please amend the paragraph beginning on line 22 of 114 as follows:

Between mammalian species, e.g. human and mouse, homologs have substantial sequence similarity, i.e. at least 75% sequence identity between nucleotide sequences. Sequence similarity is calculated based on a reference sequence, which can be a subset of a larger sequence, such as a conserved motif, coding region, flanking region, etc. A reference sequence will usually be at least about 18 nt long, more usually at least about 30 nt long, and can extend to the complete sequence that is being compared. Algorithms for sequence analysis are known in the art, such as BLAST, described in Altschul et al., (1990) *J. Mol. Biol.* 215:403-10. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (www.ncbi.nlm.nih.gov/
<http://www.ncbi.nlm.nih.gov/>).